RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/674, 377A_

Source: _PCT09_

Date Processed by STIC: _7/5/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: 09/674,377A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
 Wrapped Aminos was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
 prevent "wrapping."

2____Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
 Numbering use space characters, instead.

4____Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
 ensure your subsequent submission is saved in ASCII text.

5____Variable Length Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules,
 each n or Xaa can only represent a single residue. Please present the maximum number of each
 residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
 "bug" sequences(s) _____. Normally, PatentIn would automatically generate this section from the
 previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
 the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
 Artificial or Unknown sequences.**

7____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000

9 _✓_Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
 is Artificial Sequence

11____Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
 "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
 "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
 listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/674,377A   TIME: 10:45:27

Input Set : **A:\Q61434seq.app**
Output Set: **N:\CRF3\07052001\I674377A.raw**

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        3 <110> APPLICANT: Nakamura, Toshikazu
        5 <120> TITLE OF INVENTION: Neovascularization Inhibitors
        7 <130> FILE REFERENCE: Q61434
C-->    9 <140> CURRENT APPLICATION NUMBER: US/09/674,377A
C-->   10 <141> CURRENT FILING DATE: 2000-10-30
       12 <150> PRIOR APPLICATION NUMBER: PCT/JP99/01834
       13 <151> PRIOR FILING DATE: 1999-04-06
       15 <150> PRIOR APPLICATION NUMBER: JP 1998/134681
       16 <151> PRIOR FILING DATE: 1998-04-28
       18 <160> NUMBER OF SEQ ID NOS: 2
       20 <170> SOFTWARE: PatentIn Ver. 2.1
       22 <210> SEQ ID NO: 1
       23 <211> LENGTH: 447
       24 <212> TYPE: PRT
       25 <213> ORGANISM: Homo sapiens
       27 <220> FEATURE:
       28 <221> NAME/KEY: MOD_RES
       29 <222> LOCATION: (1)
       30 <223> OTHER INFORMATION: pyroglutamate
       32 <220> FEATURE:
       33 <221> NAME/KEY: CHAIN
       34 <222> LOCATION: (1)..(447)
       35 <223> OTHER INFORMATION: N-terminal region of alpha-chain in HGF
       36       (PyrGlu32-Val478/HGF)
       38 <300> PUBLICATION INFORMATION:
       39 <301> AUTHORs: Nakamura, Toshikazu
       40 <303> JOURNAL: Nature
       41 <304> VOLUME: 342
       42 <306> PAGES: 440-443
       43 <307> DATE: 1989
       45 <400> SEQUENCE: 1
W-->   46 Xaa Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys
       47  1               5                  10                  15
       49 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys
       50             20                  25                  30
       52 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
       53         35                  40                  45
       55 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
       56     50                  55                  60
       58 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
       59  65                  70                  75                  80
       61 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
       62                  85                  90                  95
       64 Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
       65             100                 105                 110
       67 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu
       68             115                 120                 125
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Input Set : A:\Q61434seq.app
Output Set: N:\CRF3\07052001\I674377A.raw

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70  His Ser Phe Leu Pro Ser Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn
71      130                 135                 140
73  Tyr Cys Arg Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr
74  145                 150                 155                 160
76  Ser Asn Pro Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser
77                  165                 170                 175
79  Glu Val Glu Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met
80                  180                 185                 190
82  Asp His Thr Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr
83              195                 200                 205
85  Pro His Arg His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe
86      210                 215                 220
88  Asp Asp Asn Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys
89  225                 230                 235                 240
91  Tyr Thr Leu Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr
92                  245                 250                 255
94  Cys Ala Asp Asn Thr Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr
95                  260                 265                 270
97  Glu Cys Ile Gln Gly Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr
98              275                 280                 285
100 Ile Trp Asn Gly Ile Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His
101     290                 295                 300
103 Glu His Asp Met Thr Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu
104 305                 310                 315                 320
106 Asn Tyr Cys Arg Asn Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr
107             325                 330                 335
109 Thr Asp Pro Asn Ile Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys
110             340                 345                 350
112 Asp Met Ser His Gly Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr
113             355                 360                 365
115 Met Gly Asn Leu Ser Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp
116     370                 375                 380
118 Asp Lys Asn Met Glu Asp Leu His Arg His Ile Phe Trp Glu Pro Asp
119 385                 390                 395                 400
121 Ala Ser Lys Leu Asn Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala
122             405                 410                 415
124 His Gly Pro Trp Cys Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr
125             420                 425                 430
127 Cys Pro Ile Ser Arg Cys Glu Gly Asp Thr Thr Pro Thr Ile Val
128             435                 440                 445
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 442
133 <212> TYPE: PRT
134 <213> ORGANISM: Homo sapiens
136 <220> FEATURE:
137 <221> NAME/KEY: CHAIN
138 <222> LOCATION: (1)..(442)
139 <223> OTHER INFORMATION: N-terminal region of alpha-chain in HGF
140       (PyrGlu32-Val478/HGF)
```

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Input Set : A:\Q61434seq.app
Output Set: N:\CRF3\07052001\I674377A.raw

*see item #9 m
error summary sheet.*

```
142 <220> FEATURE:
143 <221> NAME/KEY: MOD_RES
144 <222> LOCATION: (130)..(131)
145 <223> OTHER INFORMATION: deletion of 5 amino acids
147 <400> SEQUENCE: 2
W--> 148 Xaa Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys
149  1                   5                  10                  15
151 Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys
152             20                  25                  30
154 Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly
155         35                  40                  45
157 Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln
158         50                  55                  60
160 Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu
161  65                  70                  75                  80
163 Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn
164             85                  90                  95
166 Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr
167             100                 105                 110
169 Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu
170         115                 120                 125
172 His Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro
173         130                 135                 140
175 Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val
176 145                 150                 155                 160
178 Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met
179             165                 170                 175
181 Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser
182         180                 185                 190
184 Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys
185         195                 200                 205
187 Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys
188         210                 215                 220
190 Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro
191 225                 230                 235                 240
193 His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Asn Thr
194         245                 250                 255
196 Met Asn Asp Thr Asp Val Pro Leu Glu Thr Thr Glu Cys Ile Gln Gly
197         260                 265                 270
199 Gln Gly Glu Gly Tyr Arg Gly Thr Val Asn Thr Ile Trp Asn Gly Ile
200         275                 280                 285
202 Pro Cys Gln Arg Trp Asp Ser Gln Tyr Pro His Glu His Asp Met Thr
203         290                 295                 300
205 Pro Glu Asn Phe Lys Cys Lys Asp Leu Arg Glu Asn Tyr Cys Arg Asn
206 305                 310                 315                 320
208 Pro Asp Gly Ser Glu Ser Pro Trp Cys Phe Thr Thr Asp Pro Asn Ile
209         325                 330                 335
211 Arg Val Gly Tyr Cys Ser Gln Ile Pro Asn Cys Asp Met Ser His Gly
212         340                 345                 350
```

```
214 Gln Asp Cys Tyr Arg Gly Asn Gly Lys Asn Tyr Met Gly Asn Leu Ser
215         355             360             365
217 Gln Thr Arg Ser Gly Leu Thr Cys Ser Met Trp Asp Lys Asn Met Glu
218     370             375             380
220 Asp Leu His Arg His Ile Phe Trp Glu Pro Asp Ala Ser Lys Leu Asn
221 385             390             395             400
223 Glu Asn Tyr Cys Arg Asn Pro Asp Asp Asp Ala His Gly Pro Trp Cys
224         405             410             415
226 Tyr Thr Gly Asn Pro Leu Ile Pro Trp Asp Tyr Cys Pro Ile Ser Arg
227         420             425             430
229 Cys Glu Gly Asp Thr Thr Pro Thr Ile Val
230     435             440
```

VERIFICATION SUMMARY   DATE: 07/05/2001
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L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:148 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2